

Application No.: 09/15876

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RESULT 1
 S60896
 agglutinin-like protein (Candida albicans)
 C:Species: Candida albicans
 C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1997
 C:Accession: S60896
 R:Hoyer, L.L.; Scherer, S.; Shatzman, A.R.; Livi, G.P.
 Mol. Microbiol. 15, 39-54, 1995
 A:Title: Candida albicans ALS1: domains related to a Saccharomyces cerevisiae sexual
 A:Reference number: S60896; MUID:95272392
 A:Accession: S60896
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1260 <HOY>
 A:Cross-references: EMBL:L25902; NID:g704426; PIDN:AAC41649.1; PID:g704427
 C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosida

S60 ID NO: 8.

Query Match 100.0%; Score 6495; DB 2; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 1.7e-273;
 Matches 1260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQQFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPYPTWNAVGLWSLDGTS 60
 Db 1 MLQQFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPYPTWNAVGLWSLDGTS 60
 Qy 61 ANPGDTFTLNMPGVFKYTTSTQSVDLTADGVKYATCFYSGEFTTFTLTCTVNDALKS 120
 Db 61 ANPGDTFTLNMPGVFKYTTSTQSVDLTADGVKYATCFYSGEFTTFTLTCTVNDALKS 120
 Qy 121 SIKAFGTVTLPIAFNVGGTGSSTDLSDSKCFTAGTNTVTFTNDGDKDISIDVEFEKSTVDP 180
 Db 121 SIKAFGTVTLPIAFNVGGTGSSTDLSDSKCFTAGTNTVTFTNDGDKDISIDVEFEKSTVDP 180
 Qy 181 SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLND 240
 Db 181 SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLND 240
 Qy 241 WNYPVSSSESFSYTKTCTSNIGIQIKYQNVYPAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
 Db 241 WNYPVSSSESFSYTKTCTSNIGIQIKYQNVYPAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
 Qy 301 SRLQSKPFTLRWTGYKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIEILQ 360
 Db 301 SRLQSKPFTLRWTGYKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIEILQ 360
 Qy 361 PIPTTTITTSYGVVTTSYLTKTAPIGETATVIVDVPYHTTTTITSEWTGTTTTTTRTNP 420
 Db 361 PIPTTTITTSYGVVTTSYLTKTAPIGETATVIVDVPYHTTTTITSEWTGTTTTTTRTNP 420
 Qy 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTTVPAPGGTDTVIIREPPNHTVTTTEYW 480
 Db 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTTVPAPGGTDTVIIREPPNHTVTTTEYW 480
 Qy 481 SQSFATTTTVPAPGGTDSVIIREPPNPTVTTTEYWSQSFATTTTVPAPGGTDSVIIRE 540
 Db 481 SQSFATTTTVPAPGGTDSVIIREPPNPTVTTTEYWSQSFATTTTVPAPGGTDSVIIRE 540
 Qy 541 PPNPTVTTTEYWSQSYATTTTVPAPGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVA 600
 Db 541 PPNPTVTTTEYWSQSYATTTTVPAPGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVA 600
 Qy 601 PPGGTDVIIREPPNHTVTTTEYWSQSFATTTTVPAPGGTDTVIIREPPNPTVTTTEYW 660
 Db 601 PPGGTDVIIREPPNHTVTTTEYWSQSFATTTTVPAPGGTDTVIIREPPNPTVTTTEYW 660
 Qy 661 SQSYATTTTITAPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVPAPGETDTVLIRE 720
 Db 661 SQSYATTTTITAPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVPAPGETDTVLIRE 720
 Qy 721 PPNHTVTTTEYWSQSYATTTTVPAPGGTDTVIIREPPNPTVTTTEYWSQSFATTTTVA 780
 Db 721 PPNHTVTTTEYWSQSYATTTTVPAPGGTDTVIIREPPNPTVTTTEYWSQSFATTTTVA 780
 Qy 781 PPGGTDVIIYESHSSKISTSSNDITSIIPSFSRPHYVNSTSDLSFESSMNTPTSI 840
 Db 781 PPGGTDVIIYESHSSKISTSSNDITSIIPSFSRPHYVNSTSDLSFESSMNTPTSI 840
 Qy 841 SSDGMLLSSTTLVTESETTELICSDGKECSRLSSSGIVTNPDSNESSIVTSTVPTAST 900
 Db 841 SSDGMLLSSTTLVTESETTELICSDGKECSRLSSSGIVTNPDSNESSIVTSTVPTAST 900
 Qy 901 MSDLSSTDGIATSSDNVSKSGSVTTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSE 960
 Db 901 MSDLSSTDGIATSSDNVSKSGSVTTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSE 960
 Qy 961 SESKVTFTSNGDNQSGTHDSQSTSTEIEIVTTSSTKVLPPVSSNTDLTSEPTNTREQPT 1020
 Db 961 SESKVTFTSNGDNQSGTHDSQSTSTEIEIVTTSSTKVLPPVSSNTDLTSEPTNTREQPT 1020
 Qy 1021 TLSTTSNSITEDITTSOPTGDNNDNTSSTNPVPTVATSTLASASEEDNKGSHASASTSL 1080
 Db 1021 TLSTTSNSITEDITTSOPTGDNNDNTSSTNPVPTVATSTLASASEEDNKGSHASASTSL 1080
 Qy 1081 KPSMGNSGLTTSTEIEATTTSPTEAPSPAVSSGTDVTEPTDREOPTTLSTTSKTNSE 1140
 Db 1081 KPSMGNSGLTTSTEIEATTTSPTEAPSPAVSSGTDVTEPTDREOPTTLSTTSKTNSE 1140
 Qy 1141 LVATTQATNENGKSPSTDLTSSLTGTASTSANSELVTSVGTGGAVASANDQSHST 1200
 Db 1141 LVATTQATNENGKSPSTDLTSSLTGTASTSANSELVTSVGTGGAVASANDQSHST 1200
 Qy 1201 SVTNSNSIVSNTPQTTLSQQVTSPPSTNTFIASDYDGSIGIIQHSWLYGLITLLSLFI 1260
 Db 1201 SVTNSNSIVSNTPQTTLSQQVTSPPSTNTFIASDYDGSIGIIQHSWLYGLITLLSLFI 1260